

SEQUENCE LISTING

<110> TAKAKURA, Yoshimitsu et al.

<120> A NOVEL PROTEIN, A GENE CODING THEREFOR AND A METHOD OF USING THE SAME

<130> 0230-0157P

<140> 09/856,327

<141> 2001-05-21

<160> 12

<170> PatentIn version 3.1

<210> 1

<211> 2106

<212> DNA

<213> Lyophyllum shimeji

<220>

<221> CDS

<222> (8)..(1861)

<223>

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tct atg caa atc aac gga cag att cct aag aac gca att cac gaa aca 97

Ser Met Gln Ile Asn Gly Gln Ile Pro Lys Asn Ala Ile His Glu Thr

15

20

25

30

tac gga aac gac gga gtt gat gta ttc att gca gga tct gga ccc att 145

Tyr Gly Asn Asp Gly Val Asp Val Phe Ile Ala Gly Ser Gly Pro Ile

35

40

45

gga gcg acg tat gca aag ctc tgt gtt gaa gct ggt cta cgt gtt gtg 193

Gly Ala Thr Tyr Ala Lys Leu Cys Val Glu Ala Gly Leu Arg Val Val

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55

60

atg gtc gag atc gga gct gct gat agc ttc tac gct gtt aat gcc gaa 241

Met Val Glu Ile Gly Ala Ala Asp Ser Phe Tyr Ala Val Asn Ala Glu

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70

75

gaa gga act gca gtt ccc tac gtt cct ggc tac cac aag aag aat gaa 289

Glu Gly Thr Ala Val Pro Tyr Val Pro Gly Tyr His Lys Lys Asn Glu

80

85

90

atc gag ttc cag aaa gat att gac cgc ttc gtc aat gta atc aag gga 337

Ile Glu Phe Gln Lys Asp Ile Asp Arg Phe Val Asn Val Ile Lys Gly

95

100

105

110



gcc tta caa caa gtc tct gtt cct gtc aga aac cag aac gtg cct aca 385
Ala Leu Gln Gln Val Ser Val Pro Val Arg Asn Gln Asn Val Pro Thr
115 120 125

ctt gat ccc gga gcc tgg agc gcg ccc cct gga agt tca gcc ata tcg 433
Leu Asp Pro Gly Ala Trp Ser Ala Pro Pro Gly Ser Ser Ala Ile Ser
130 135 140

aac ggt aaa aat cct cac cag cgg gaa ttc gag aac ttg tct gcg gag 481
Asn Gly Lys Asn Pro His Gln Arg Glu Phe Glu Asn Leu Ser Ala Glu
145 150 155

gcc gta acg cgt gga gtc ggc ggc atg agt acc cac tgg acg tgc tcc 529
Ala Val Thr Arg Gly Val Gly Gly Met Ser Thr His Trp Thr Cys Ser
160 165 170

acg cca cgg att cat cca ccc atg gaa agt ctc ccg ggc atc ggc cgt 577
Thr Pro Arg Ile His Pro Pro Met Glu Ser Leu Pro Gly Ile Gly Arg
175 180 185 190

ccg aag ctc agt aac gac ccg gca gag gac gac aaa gag tgg aac gag 625
Pro Lys Leu Ser Asn Asp Pro Ala Glu Asp Asp Lys Glu Trp Asn Glu
195 200 205

ctt tat tcc gag gcc gag cgt ctc atc ggg act tcc acc aag gaa ttc 673
Leu Tyr Ser Glu Ala Glu Arg Leu Ile Gly Thr Ser Thr Lys Glu Phe
210 215 220

gac gag tca att cgg cac acc ctt gtt ctg cgc tct ttg caa gac gcg 721
Asp Glu Ser Ile Arg His Thr Leu Val Leu Arg Ser Leu Gln Asp Ala
225 230 235

tac aag gat cgt caa cgt atc ttt cgc cct ctc ccg ttg gca tgc cac 769
Tyr Lys Asp Arg Gln Arg Ile Phe Arg Pro Leu Pro Leu Ala Cys His
240 245 250

cgg ttg aag aac gcg ccg gaa tac gtc gaa tgg cac tca gca gaa aat 817
Arg Leu Lys Asn Ala Pro Glu Tyr Val Glu Trp His Ser Ala Glu Asn
255 260 265 270

ctt ttc cac tct atc tac aac gat gac aag cag aag aag ctc ttt acc 865
Leu Phe His Ser Ile Tyr Asn Asp Asp Lys Gln Lys Lys Leu Phe Thr
275 280 285

ctg ctg acg aac cat cgc tgc aca cga ctg gcg ctt acg ggc ggg tat 913
Leu Leu Thr Asn His Arg Cys Thr Arg Leu Ala Leu Thr Gly Gly Tyr
290 295 300

gag aag aag att ggc gct gcc gag gtc agg aat cta ctg gcc acc agg 961
Glu Lys Lys Ile Gly Ala Ala Glu Val Arg Asn Leu Leu Ala Thr Arg
305 310 315

aat cct agt tcg cag ctg gac agc tat atc atg gcg aag gta tat gta 1009
Asn Pro Ser Ser Gln Leu Asp Ser Tyr Ile Met Ala Lys Val Tyr Val
320 325 330

ctg gcg tcg gga gcg atc ggc aac cca cag att ctc tat aac tcg ggc	1057
Leu Ala Ser Gly Ala Ile Gly Asn Pro Gln Ile Leu Tyr Asn Ser Gly	
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ttc tct ggg cta cag gtc acg cca cgc aat gac tcg ttg atc ccc aac	1105
Phe Ser Gly Leu Gln Val Thr Pro Arg Asn Asp Ser Leu Ile Pro Asn	
355 360 365	
ctg ggg agg tac atc acg gag cag ccg atg gca ttt tgc cag ata gtc	1153
Leu Gly Arg Tyr Ile Thr Glu Gln Pro Met Ala Phe Cys Gln Ile Val	
370 375 380	
ttg agg cag gaa ttc gtc gac agc gtg cgc gac gat cct tat gga ctg	1201
Leu Arg Gln Glu Phe Val Asp Ser Val Arg Asp Asp Pro Tyr Gly Leu	
385 390 395	
cca tgg tgg aaa gaa gcc gtt gct caa cat att gcc aag aac ccg aca	1249
Pro Trp Trp Lys Glu Ala Val Ala Gln His Ile Ala Lys Asn Pro Thr	
400 405 410	
gat gca ctg ccc att ccg ttc cgc gat ccg gaa ccc cag gta aca acc	1297
Asp Ala Leu Pro Ile Pro Phe Arg Asp Pro Glu Pro Gln Val Thr Thr	
415 420 425 430	
cca ttt aca gaa gaa cac ccc tgg cac acg cag att cac cgc gat gct	1345
Pro Phe Thr Glu Glu His Pro Trp His Thr Gln Ile His Arg Asp Ala	
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ttt tcg tac ggt gcc gtc ggt cct gag gtg gac tct cgt gtc atc gtc	1393
Phe Ser Tyr Gly Ala Val Gly Pro Glu Val Asp Ser Arg Val Ile Val	
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gac ctg cgc tgg ttt ggc gca acc gac cct gaa gca aac aac ctt ttg	1441
Asp Leu Arg Trp Phe Gly Ala Thr Asp Pro Glu Ala Asn Asn Leu Leu	
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gtt ttc cag aac gat gtt caa gac ggg tac agt atg ccg cag ccg acg	1489
Val Phe Gln Asn Asp Val Gln Asp Gly Tyr Ser Met Pro Gln Pro Thr	
480 485 490	
ttc aga tat cga ccc agc act gcg tca aac gtg aga gca agg aaa atg	1537
Phe Arg Tyr Arg Pro Ser Thr Ala Ser Asn Val Arg Ala Arg Lys Met	
495 500 505 510	
atg gcc gat atg tgc gaa gtg gcg agc aac ttg gga ggt tat ttg ccc	1585
Met Ala Asp Met Cys Glu Val Ala Ser Asn Leu Gly Gly Tyr Leu Pro	
515 520 525	
acg tcc ccc ccg cag ttt atg gat cca ggc ctt gca ctt cat ctt gcg	1633
Thr Ser Pro Pro Gln Phe Met Asp Pro Gly Leu Ala Leu His Leu Ala	
530 535 540	
ggg act act cgc att ggc ttc gac aag gca act aca gtg gct gat aac	1681
Gly Thr Thr Arg Ile Gly Phe Asp Lys Ala Thr Thr Val Ala Asp Asn	
545 550 555	

aac tcg ctg gtc tgg gac ttt gcc aat ctt tat gtt gca ggc aat ggc 1729
 Asn Ser Leu Val Trp Asp Phe Ala Asn Leu Tyr Val Ala Gly Asn Gly
 560 565 570

acc atc agg acg ggc ttc ggc gag aac ccg aca ctt acg tcg atg tgc 1777
 Thr Ile Arg Thr Gly Phe Gly Glu Asn Pro Thr Leu Thr Ser Met Cys
 575 580 585 590

cac gct atc aag agc gcg agg agc atc atc aat aca ctc aag ggt ggg 1825
 His Ala Ile Lys Ser Ala Arg Ser Ile Ile Asn Thr Leu Lys Gly Gly
 595 600 605

act gac gga aaa aat aca ggc gag cat cgc aac ctt tgaggaagga 1871
 Thr Asp Gly Lys Asn Thr Gly Glu His Arg Asn Leu
 610 615

gcaacagcag tgtaaacaaa cgcgtcaagt ggctacttca agttgaatgc attctgggtcc 1931

cctaccatgt tgatgtgtac gataggcggtt gaaagatttt gtgtattact gaacctgtac 1991

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 <213> Lyophyllum shimeji

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Asn Asp Gly Val Asp Val Phe Ile Ala Gly Ser Gly Pro Ile Gly Ala
 35 40 45

Thr Tyr Ala Lys Leu Cys Val Glu Ala Gly Leu Arg Val Val Met Val
 50 55 60

Glu Ile Gly Ala Ala Asp Ser Phe Tyr Ala Val Asn Ala Glu Glu Gly
 65 70 75 80

Thr Ala Val Pro Tyr Val Pro Gly Tyr His Lys Lys Asn Glu Ile Glu
 85 90 95

Phe Gln Lys Asp Ile Asp Arg Phe Val Asn Val Ile Lys Gly Ala Leu
100 105 110

Gln Gln Val Ser Val Pro Val Arg Asn Gln Asn Val Pro Thr Leu Asp
115 120 125

Pro Gly Ala Trp Ser Ala Pro Pro Gly Ser Ser Ala Ile Ser Asn Gly
130 135 140

Lys Asn Pro His Gln Arg Glu Phe Glu Asn Leu Ser Ala Glu Ala Val
145 150 155 160

Thr Arg Gly Val Gly Gly Met Ser Thr His Trp Thr Cys Ser Thr Pro
165 170 175

Arg Ile His Pro Pro Met Glu Ser Leu Pro Gly Ile Gly Arg Pro Lys
180 185 190

Leu Ser Asn Asp Pro Ala Glu Asp Asp Lys Glu Trp Asn Glu Leu Tyr
195 200 205

Ser Glu Ala Glu Arg Leu Ile Gly Thr Ser Thr Lys Glu Phe Asp Glu
210 215 220

Ser Ile Arg His Thr Leu Val Leu Arg Ser Leu Gln Asp Ala Tyr Lys
225 230 235 240

Asp Arg Gln Arg Ile Phe Arg Pro Leu Pro Leu Ala Cys His Arg Leu
245 250 255

Lys Asn Ala Pro Glu Tyr Val Glu Trp His Ser Ala Glu Asn Leu Phe
260 265 270

His Ser Ile Tyr Asn Asp Asp Lys Gln Lys Lys Leu Phe Thr Leu Leu
275 280 285

Thr Asn His Arg Cys Thr Arg Leu Ala Leu Thr Gly Gly Tyr Glu Lys
290 295 300

Lys Ile Gly Ala Ala Glu Val Arg Asn Leu Leu Ala Thr Arg Asn Pro
305 310 315 320

Ser Ser Gln Leu Asp Ser Tyr Ile Met Ala Lys Val Tyr Val Leu Ala
325 330 335

Ser Gly Ala Ile Gly Asn Pro Gln Ile Leu Tyr Asn Ser Gly Phe Ser
340 345 350

Gly Leu Gln Val Thr Pro Arg Asn Asp Ser Leu Ile Pro Asn Leu Gly
355 360 365

Arg Tyr Ile Thr Glu Gln Pro Met Ala Phe Cys Gln Ile Val Leu Arg
370 375 380

Gln Glu Phe Val Asp Ser Val Arg Asp Asp Pro Tyr Gly Leu Pro Trp
385 390 395 400

Trp Lys Glu Ala Val Ala Gln His Ile Ala Lys Asn Pro Thr Asp Ala
405 410 415

Leu Pro Ile Pro Phe Arg Asp Pro Glu Pro Gln Val Thr Thr Pro Phe
420 425 430

Thr Glu Glu His Pro Trp His Thr Gln Ile His Arg Asp Ala Phe Ser
435 440 445

Tyr Gly Ala Val Gly Pro Glu Val Asp Ser Arg Val Ile Val Asp Leu
450 455 460

Arg Trp Phe Gly Ala Thr Asp Pro Glu Ala Asn Asn Leu Leu Val Phe
465 470 475 480

Gln Asn Asp Val Gln Asp Gly Tyr Ser Met Pro Gln Pro Thr Phe Arg
485 490 495

Tyr Arg Pro Ser Thr Ala Ser Asn Val Arg Ala Arg Lys Met Met Ala
500 505 510

Asp Met Cys Glu Val Ala Ser Asn Leu Gly Gly Tyr Leu Pro Thr Ser
515 520 525

Pro Pro Gln Phe Met Asp Pro Gly Leu Ala Leu His Leu Ala Gly Thr
530 535 540

Thr Arg Ile Gly Phe Asp Lys Ala Thr Thr Val Ala Asp Asn Asn Ser
545 550 555 560

Leu Val Trp Asp Phe Ala Asn Leu Tyr Val Ala Gly Asn Gly Thr Ile
565 570 575

Arg Thr Gly Phe Gly Glu Asn Pro Thr Leu Thr Ser Met Cys His Ala
580 585 590

Ile Lys Ser Ala Arg Ser Ile Ile Asn Thr Leu Lys Gly Gly Thr Asp
595 600 605

Gly Lys Asn Thr Gly Glu His Arg Asn Leu
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Lys Asn Glu Ile Glu Phe Gln Lys Asp Ile Asp Arg Phe Val
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Asp Ala Tyr Lys Asp Arg Gln Arg
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Arg His Thr Leu Val Leu Arg Ser Leu Gln Asp Ala Tyr
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Arg His Thr Leu Val Leu Arg Ser Leu Gln Asp Ala Tyr Lys Asp Arg
 20 25 30

Gln Arg

<210> 7
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 <223> n represents inosine

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<210> 8
 <211> 23
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<220>
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<400> 8
 garttycara argayathga ymg

23

<210> 9
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 <220>
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<400> 9
 ttygtnaayg tnathtgygg ngc 23

<210> 10
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 <222> (1)..(23)
 <223> n represents inosine

<400> 10
 tgnckdatns wytcrtrcaa ytc 23

<210> 11
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 <213> Artificial Sequence

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 <222> (1)..(23)
 <223> n represents inosine

<400> 11
 tgnckrtcyt trtangcrtc ytg 23

<210> 12
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B1
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Concludes

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<222> (1)..(23)
<223> n represents inosine

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ggngcraada tnckytgnck rtc

23

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